

FIG.1

ADAMTS-E nucleotide sequence [SEQ ID NO: 1]

CACGCGTCCGACGGCGCGGAGGCCCGGGCGCGCAGGAGCCCGGTGAT  
5 GCTGCGAAGGCTGTGAACAGGGAGGGCGACTGTGGGGCTGCCGCAGCGGGG  
CTGGGGAGAGACATGTGGACACGTGGCTCATGGCTCCCGCTGCCAGATCCCGC  
TGGGCCCTCCGCCCTGGGCTGGCCTCATGTTGAGGTACGCACGCCCTCCGGTCTC  
AAGATGAGTTCCTGTCCAGTCTGGAGAGCTATGAGATCGCCTCCCCACCCGCGTGAC  
CACAAACGGGGCACTGCTGCCCTCTGCCACCTCCTCCCCGGAGGCAGCGCCCGGC  
10 ACGGGGGCCACAGCGAGTCCCACCTTACAAGTGGCTGCCAGCACCCACT  
TCCTGCTGAACCTGACCCCGAGCTCCCGTACTGGCAGGGCACGTCTCCGTGGAGTA  
CTGGACACGGGAGGGCCTGGCAGAGGGCGCCCGGCCCCACTGCCTACGC  
TGGTCACCTGCAGGGCCAGGCCAGCACCTCCATGTGGCCATCAGCACCTGTGGAGGC  
CTGCACGGCCTGATCGTGGCAGACGAGGAAGAGTACCTGATTGAGCCCCTGCACGGTG  
15 GGCCCAAGGGTCTCGAGCCCGAGGAAAGTGGACCACATGGGTGTACAAGCGTT  
CTCTCGCTCACCCCCACCTGGACACAGCCTGTGGAGTGAGAGATGAGAACCGTGG  
AAAGGGCGGGCATGGTGGCTGGGACCTGAAGCCACCGCCTGCCAGGCCCCCTGGGG  
AATGAAACAGAGCGTGGCCAGCCAGGCCGAAGCGATCGGTAGCCGAGAGCGCTACG  
TGGAGACCCCTGGTGGCTGACAAGATGATGGTGGCCTATCACGGGCGCCGGGATGT  
20 GGAGCAGTATGTCCTGCCATCATGAAACATTGTTGCAAACATTCCAGGACTCGAGTC  
GGGAAGCACCGTTAACATCCTCGTAACTCGCCTCATCTGCTCACGGAGGACCAGCCCA  
CTCTGGAGATCACCCACCATGCCGGAAAGTCCCTGGACAGCTCTGTAAGTGGCAGAAA  
TCCATCGTGAACCACAGCGGCCATGGCAATGCCATTCCAGAGAACGGTGTGGCTAACCA  
TGACACAGCAGTGTCTACACGCTATGACATCTGCATCTACAAGAACAAACCTCGC  
25 GCACACTAGGCCCTGGCCCCGGTGGCGGAATGTGTAGCGCGAGAGAACGCTCGAGCG  
TCAATGAGGACATTGGCTGGCCACAGCGTTACCATGGCCACAGGAGATCGGCACACA  
TTCGGCATGAACCATGACGGCGTGGGAAACAGCTGTGGGCCCCGTGGTCAAGGACCCAG  
CCAAGCTATGGCTGCCACATTACCATGAAAGACCAACCCATTGCGTGGTCACTCTGC  
AGCCGTGACTACATCACCAGCTTCTAGACTCGGGCTGGGCTTGCCCTAACACCG  
30 GCCCCCCAGACAGGACTTGTGTACCCGACAGTGGCACCGGGCAAGCCTACGATGCA  
GATGAGCAATGCCCTTCACTGGAGTCAAATCGCGTCAGTGAAATACGGGGAGGT  
CTGCAGCGAGCTGTGGTCTGAGCAAGCAACCGGTGCATACCAACAGCATCCCG  
GCCGCCAGGGCACGCTGTGCCAGAGCACCACATGACAAGGGGTGGTCAACAAAC  
GGGTCTGTGCCCCCTTGGTCGCGCCCAAGAGGGTGTGGACGGAGCCTGGGGCGT  
35 GGACTCCATGGGCGACTGCAGCCGGACCTGTGGCGCGCGTGTCTCTTAGCC  
GTCACTGCGACAGCCCCAGGCCAACCATGGGGCAAGTACTGTCTGGGTGAGAGAAG  
CGGGCACCGCTCTGCAACACGGATGACTGTCCCCCTGGCTCCAGGACTTCAGAGAA

EXPRESS MAIL NO. E 144648267 US

GTGCAGTGTTCTGAATTGACAGCATCCCTTCCGTGGAAATTCTACAAGTGGAAAACG  
TACCGGGGAGGGGGCGTGAAGGCCTGCGTCACCGCCTAGCGGAAGGCTCAACT  
TCTACACGGAGGGCGGCAGCCGTGGTGGACGGGACACCCCTGCCGTCCAGACACGG  
TGGACATTGCGTCAGTGGCGAATGCAAGCACGTGGCTGCGACCGAGTCCTGGCTC  
5 CGACCTCGGGAGGACAAGTGCAGTGTGCGGTGACGGCAGTGCCTGCGAGAC  
CATCGAGGGCGTCTCAGCCCAGCCTCACCTGGGGCGGGTACGAGGATGTCGCTGG  
ATTCCCAAAGGCTCGTCCACATCTCATCCAGGATCTGAACCTCTCTCAGTCACTTG  
GCCCTGAAGGGAGACCAGGAGTCCCTGCTGCTGGAGGGTCCCCGGGACCCCCCAG  
CCCCACCGTCTGCCTTAGCTGGGACCACCTTCAACTGCGACAGGGCCAGACCAGG  
10 TCCAGAGCCTCGAAGCCCTGGGACCGATAATGCATCTCATCGTCATGGTCTGGCC  
CGGACCGAGCTGCCCTGCCCTCGTACCGCTTAATGCCCGATCGCCGTGACTCGC  
TGCCCCCCTACTCCTGGCACTATGCGCCCTGGACCAAGTGCTCGGCCAGTGTGCAAGG  
CGGTAGCCAGGTGCAGGGGTGGAGTGCGCAACCAGCTGGACAGCTCCGCGGTGCG  
CCCCCACTACTGCAGTGCCACAGCAAGCTGCCAAAGGCAGCGCCCTGCAACACG  
15 GAGCCTGCCCTCCAGACTGGTTGTAGGGAACTGGTCGCTCTGAGCCGAGCTGCG  
ATGCAGGGCGTGCAGCCGCTCGGTGCGCCAGCGCCGCGTCTGCCCGGGAGG  
AGAAGGGCGTGGACGACAGCCATGCCCGAGGCCGCCCCACCTGACTGGAGGCCT  
GCCACGGCCCCACTTGCCCTCCGGAGTGGCGGGCCCTGACTGGTCTGAGTGCACCC  
CCAGCTGCCGGCCGGGCGGCCACCGCGTGGTCTTGCAAGAGCGCAGACCACC  
20 GCGCCACGCTGCCCGGCGACTGCTACCCGCCAGCCACCGGCCACCATGC  
GCTGCAACTTGCAGCCGCTGCCCGCCGCTGGTGGCTGGAGTGGGTGAGT  
GCTCTGCACAGTGCAGCCGCTGGCAGCGCAGCGCTCGGTGCGCTGCACAGCCACA  
CGGGCCAGGCCTGCAAGTGCACGGAGGCCCTGCCGCGCCGACTACCACGCAGC  
AGTGTGAGGCCAAGTGCAGCCACAGCCAAACCCCGGGAGGCCCTGAAGAGTGCAGG  
25 ATGTGAACAAGGTGCCTACTGCCCTGGTCTCAAATTCTGAGCTGCAGCCGAGCC  
TACTCCGCCAGATGTGCTGCAAAACCTGCCAGGGCCACTAGGGGGCGCGGCCACCC  
GGAGGCCACAGCTGGCGGGCTCCGCCAGCCCTGAGCGGGCCGCCAGAGGG  
GGCCCCGGGGGGGGGGAGGGAACTGGGAGGGAGGTGAGACGGAGGCCGGAAGTTATT  
ATTGGGAACCCCTGCAAGGCCCTGGCTGGAGGATCCACCCCAACCTGCCCC  
30 GCCCCAGGGCACACACTCCTGCCAGGAAGCCATCAATAAGTCTGTCTTAGAT  
TTCTAAAAAAAAAAAAAA

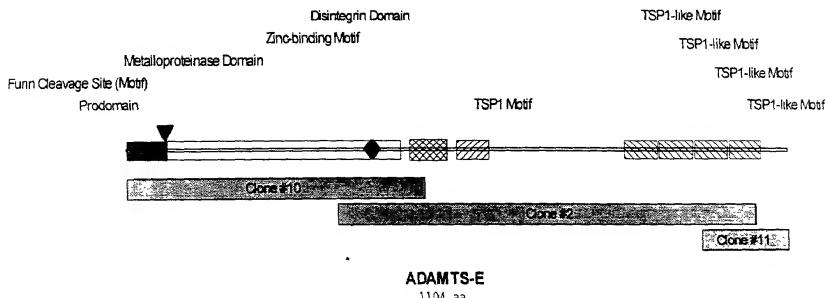
FIG 2

ADAMTS-E amino acid sequence [SEQ ID NO: 2]

MAPACQILRWALALGLGLMFEVTHAFRSQDEFLSSLESYEIAFPTRVDHNGALLAFS  
PPPPRQRRTGATAESRLFYKVASPSTHFLLNLTRSSRLLAGHVSVEWTREGLA  
WQRRAARPHCLYAGHLQQQASTSHVAISTCGGLHGLIVADEEEYLIEPLHGGPKGSR  
SPEESGPHVVYKRSSLRHPHLDTACGVRDEKPWKGRPWWRTLKPPPAPRLGNE  
TERGQPGLKRSVSRERYVETLVVADKMMVAYHGRRDVEQYVLAIMNIVAKLFQDSS  
LGSTVNILVTRLILLTEDQPTLEITHAGKSLSFCWKWQKSIVNHSGHGNAPIENGVA  
NHDTAVLITRYDICIYKNKPCGTGLAPVGMCRERSCSVNEDIGLATAFTIAHEIG  
HTFGMNHDGVGNSCGARGQDPAKLMAAHITMKTNPFWSSCSRDYITSFLDSGLG  
LCLNNRPPRQDFVYPTVAPGQAYDAEQCRFQHGVKSRQCKYGEVCSELWCLSK  
SNRCITNSIPAAEGTLQCQTHTIDKGWCYKRVCPFGSRPEGVDAWGPWTWGDC  
SRTCAGGGVSSSSRHCDSPRPTIGGKYCLGERRRHRCNTDDCOPGSQDFREVQC  
SEFDSPFGRKFYKWKTYRGGVVKACSLTCLAEGFNFYTERAAVVDGTPCRPDTV  
DICVSGECKHVGCDRVLGSDLREDKCRVCGGDGSACETIEGVFSPASPGAGYEDV  
VWIPKGSVHIFIQDLNLSLSHLALKGDQESLLEGLPGTPQPHRLPLAGTTFQLRQGP  
DQVQSLEALGPINASLIVMVLARTELPALRYRFNAPIARDSLPPYSWHYAPWTKCSA  
QCAGGSQVQAVERCRNQLDSSAVAPHYCSAHSKLPKRQRACNTEPCPPDWVGN  
WSLCRSRSCDAGVRSRSVVCQRRVSAEAEKALDDSACPQPRPPVLEACHGPTCPPE  
WAALDWSECTPSCGPGLRHRVVLCKSDAHRATLPPAHCSPAACKPATMRCNLRRC  
PPARWVAGEWGECSAQCGVGQRQRSRCTSHTGQASHECTEALRPPTTQQCE  
AKCDSPTEGDGPEECKDVNVAYCPLVLKFQFCRAYFRQMCCKTCQGH

**Figure 3. Domain structure of ADAMTS-E and translated nucleic acid sequence.** A) Diagram of ADAMTS-E showing the following domains and signature motifs (with amino acid numbers in parentheses): prodomain (1-66), furin cleavage site (63-66), metalloproteinase domain (67-453), zinc-binding motif (392-420), disintegrin domain (469-531), TSP1 motif (548-601), and four TSP1-like motifs (829-884, 888-944, 948-1002, and 1007-1058). Overlapping clones covering the indicated sequence segments are depicted at the bottom of the diagram. B) ADAMTS-E nucleotide sequence with translated amino acid sequence above.

A



B

1	CACGCGTCCG ACGGCGCGGA GGCCCCGGGC GCGGCGCAGG AGCCCGGTGA TGCTGCGAAG GCTGTGAAACA GGGGAGGCGG <u>GTGCGCAGGC TGCCGCGCCT CGGGGGCCCG CGCGCGTCC TCGGGCCACT ACCGAGGCTTC CGACACTTGT CCCCTCCCGC</u>	
+1		M A P A C Q I ----- Prodomain
81	CACTGTGGGG GCTGCCGGCA GCCGGGGCTG GGGAGAGACA TGTGGACACG TGCCCTCAT GGCTCCGCC TGCCAGATCC <u>GTGACACCCC CGACGGCGT CGGGCCCGAC CCCTCTCTGT ACACCTGTGC ACCGGAGATA CCGAGGGCGG AGGGTCTAGG</u>	
+1	L R W A L A L G L G L M F E V T H A F R S Q D E F L S ----- Prodomain	
161	TCCGCTGGGC CCTCGCCCTG GGGCTGGGCC TCATGTTCGA GGTCAACGAC GCCTTCCGGT CTCAAGATGA GTTCCCTGCC <u>AGGCGACCCG GGAGCGGGAC CCCGACCCGG AGTACAAGCT CCAGTGCCTG CGGAAGGCCA GAGTTCTACT CAAGGACAGG</u>	
+1	S L E S Y E I A F P T R V D H N G A L L A F S P P P P Prodomain	
241	AGTCTGGAGA GCTATGAGAT CGCCTTCCCC ACCCGCGTGG ACCACAACGG GGCACTGCTG GCCTTCTCGC CACCTCTCC <u>TCAGACCTCT CGATACTCTA CGGGAGGGG TGGGCGACCC TGTTGTTGCC CCCTGACGAC CGGAAGGGG GTGAGGGAGG</u>	

+1 R R Q R R G T G A T A E S R L F Y K V A S P S T A F  
 Furin Cleavage Site (Motif)  
 =====  
 Prodomain Metalloproteinase Domain  
 =====

321 CGGGAGGCAG CGCCCGCGCA CGGGGGCCAC AGCCGAGTCC CGCTCTCTCT ACAAGTGGC CTGCCCGCAGC ACCGATTCG  
GGCCTCCGTC GGGCGCCGT GCCCCCGGTG TCGGCTCAGG GCGGAGRAAGA TGTTCACCG GAGCGGGTGG TGGTGAACG

-1 L L N L T R S S R L L A G H V S V E Y W T R E G L A A  
 Metalloproteinase Domain  
 =====

401 TCGTGAACCT GACCCGACG TCCTCTACTAC TGGCAGGGCA CCTCTCCGCGT GAGTACTGGA CACGGAGGG CCTGGCTCTG  
ACGACTTGGA CTGGCGCTCG AGGGCAGATG ACCGTCCTCG GCAGAGGCAC CTCATGACCT GTGCCCTCCC GGACCGAGG

+1 Q R A A R P H C L Y A G H L Q G Q A S T S H V A I S T  
 Metalloproteinase Domain  
 =====

481 CAGAGGGGG CGCGGCCCA CTGCTCTACTAC GCTGGTCACC TCCAGGGCA GCCCAGCACCC TCCCATGTGG CCATCGAC  
GTCCTCCGCC GGGCGGGGT GACGGAGATG CGACCGATGG ACCTCCCGT CGGGTGTGG AGGTACACCC GGTAGTGCTG

+1 C G G L H G L I V A D E E E Y L I E P L H G G P K G  
 Metalloproteinase Domain  
 =====

561 CTGTGGAGGC CTGCA CGGCC TGATCGTGGC AGACGAGGAA GAGTACCTGA TTGACCCCT GCACGGTGGG CCCAGGGTT  
GACACCTCG GACGTGCCGG ACTAGCACCG TCTGCTCTT CTCATGGACT AACCTGGGA CGTGCACCC GGGTTCGACAA

+1 S R S P E E S G P H V V Y K R S S L R H P H L D T A C  
 Metalloproteinase Domain  
 =====

641 CTCGGAGGCC GGAGGAAAGT GGACCRATG TGGTGTACAA GGTTCTCTCT CGCTGTCACC CCCACCTGG CAACAGCTGT  
GAGCTCGGG CCTCCCTTCA CCTGGTGTAC ACCACATTT CGCAAGGAGA GACGCGATGG GGGTGGACCT GTGTCGACAA

+1 G V R D E K P W K G R P W W L R T L K P P P A R P L G  
 Metalloproteinase Domain  
 =====

721 GGAGTGAGG ATGAGAACCGT GTGAAAGGG CGGCATGGT GGTGCGGAC CTGGAGGCA CGGCCTGCCA CGCCGCTGGG  
CCTCACTCTC TACTCTTGG CACCTTCCC GCCGGTACCA CGCACCGCTG GAACCTGGT GGCAGGACGGT CGGGGGACCC

+1 N E T E R G Q P G L K R S V S R E R Y V E T L V V A  
 Metalloproteinase Domain  
 =====

801 GAATGAAACA GAGCGTGGCC AGCCAGGCCT GAAGCGATCG GTCAGCCGAG AGCGCTACGT GGAGACCTG GTGGTGGCTG  
CTTACTTTGT CTGGCACCGG TCGGCTCCGA CTTCGCTAGC CAGTCGGCTC TCGCGATGCA CCTCTGGAC CACCAACGAC

+1 D K M M V A Y H G R R D V E Q Y V L A I M N I V A K L  
 Metalloproteinase Domain  
 =====

881 ACAAGATGAT GGTTGGCTAT CACGGCGCC GGGATGTGGA GCAGTATGTC CTGGCCATCA TGAACTTGT TGCAAACATT  
TGTTCTACTA CCACCGGATA GTGCCCCGG CCCTACACCT CGTCATACAG GACCGTAGT ACTTGAACA ACGGTTGAA

+1 F Q D S S L G S T V N I L V T R L I L L T E D Q P T I  
Metalloproteinase Domain

=====

961 TTCCAGGACT CGAGTCTGGG AAGCACCGTT AACATCCTCG TAACTCGCCT CATCTGCTC ACGGAGGACG AGCCACCTGT  
AAGGTCTGA GCTCAGACCC TTCTGGCAA TTGTAGGAGC ATTGAGCGGA GTAGGACGAG TGCCCTGCTG TCGGGTAGC

+1 E I T H H A G K S L D S F C K W Q K S I V N H G L  
Metalloproteinase Domain

=====

1041 GGAGATCACCA CACCATGCCG GGAAAGTCCT GCACAGCTTC TGTAAGTGGC AGAACATCCAT CGTGACCCAC AGCGGCCATG  
CCTCTAGTGG GTGGTACGCC CCTTCAGGG CCTGTCGAG ACATTCACCG TCTTGTGTTA GCACTGGTG TCGGGGTAC

+1 G N A I P E N G V A N H D T A V L I T R Y D I C I Y K  
Metalloproteinase Domain

=====

1121 GCAATGCCAT TCCAGAGAAC GGTGTGGCTA ACCATGACAC :3CAGTGCTC ATCACACGCT ATGACATCTG CATCTACAGC  
CGTTACGGTA AGGTCTCTTG CCACACCGAT TGTTACTGTG :3CTCACGAG TAGTGTGCGA TACTCTAGAC GTAGATCTG

+1 N K P C G T L G L A P V G G M C E R E R S C S V N E D  
Metalloproteinase Domain

=====

1201 AACAAACACT CGGGCACACT AGGCCTGGCC CGGGTGGCG GAATGTGTGA GCGCGAGAGA AGCTGCAGCG TCAATGAGGA  
TTGTTGGGA CGGGTGTGA TCGGGACCGG GGCCACCCCG CCTACACACT CGCGCTCTCT TCAGCTCGC AGTTACTCT

+1 I G L A T A F T I A H E I G H T F G M N H D G V G N  
Zinc-binding Motif

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Metalloproteinase Domain

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1281 CATTGGCTG GCCACAGCGTC TCACCATTCG CCACGAGATC GGGCACACAT TCGGCATGAA CCATGACGGC GTGGGAAARCA  
GTAACCGGAC CGGTGTGCGA AGTGGTAACG GGTGCTCTAG CCCGTGTGTA AGCCGTACTT GGTAATGCG CACCCCTTGT

+1 S C G A R G Q D P A K L M A A H I T M K T N P F V W S  
Zinc-binding Motif

=====

Metalloproteinase Domain

=====

1361 GCTGTGGGC CGCTGGTCAG GACCCAGCCA AGCTCATGGC TGCCACATT ACCATGAGA CCAACCCATT CGTGTGGTCA  
CGACACCCCG GGCACCAGTC CTGGTCTGGT TCGAGTACCG ACGGGTGTRA TTGTTACTCTT GGTTGGTAA GCACACCACT

+1 S C S R D Y I T S F L D S G L G L C L N N R P P R Q D  
Metalloproteinase Domain

=====

1441 TCCCTGAGCC GTGACTACAT CACCAAGCTTT CTAGACTCGG GCCTGGGGCT CTGCCTGAAC AACCGGGCCC CGAGACAGGA  
AGGACGTGG CACTGATGTA GTGGTCGAAA GATCTGAGCC CGGACCCCGA GACGGACTTG TTGGCCGGGG GGTCTGTCT

+1 F V Y P T V A P G Q A Y D A D E Q C R F Q H G V K S  
Disintegrin Domain

=====

1521 CTTTGTGTAC CGGACAGTGG CACCGGGCCA AGCCTACGAT CGAGATGAGC ATAGCCGCTT TCAGCATGGA GTCAAATCGC  
GAAACACATG GGCTGTCACT TTGGCCCCGT TCGGATGCTA CGTCTACTCG TTACGGCGAA AGTCTGACTCT CAGTTTACCG

+1 R Q C K Y G E V C S E L W C L S K S N R C I T N S I P  
 Disintegrin Domain

=====

1601 GTCAGTGTAA ATACGGGGAG GCTCGCAGCG AGCTGTGGTG TCTGAGCAAG AGCAACCGT GCATCACCAA CAGCATGCC  
CAGTCACATT TATGCCCTCC CAGACGTCGC TCGCACACCAG AGACTCGTTC TCGTTGGCCA CGTAGTGGTT GCGCTGCC

+1 A A E G T L C Q T H T I D K G W C Y K R V C V ? F S S  
 Disintegrin Domain

=====

1681 GCCGGCGAGG GCACGCTGTG CCAGACGCAC ACCATCGACA AGGGGTGGTG CTACAAACGG GTCTGTGTC COTTGGGTC  
CGCGCGCTCC CGTGCACAC GGTCTCGGTG TGGTAGCTGT TCCCCAACAC GATGTTGCC CAGACACAGG GGAAACCG

+1 R P E G V D G A W G P W T P W G D C S R T C G G S V  
 TSP1 Motif

=====

1761 GCGCCCAGAG GGTGTGGAGC GAGCTGGGG GCGCTGGACT CCATGGGGG ACTGCAGCG GACCTGTGGC GCGGGCGGT  
CGCGGGTCTC CCACACCTGC CTCGGACCCC CGGCACCTGA GGTAACCCCG TGACGTCGCC CTGGACACCG CGCGCACAC

+1 S S S S R H C D S P R P T I G G K Y C L G E R R R R H R  
 TSP1 Motif

=====

1841 CCTCTCTAG CGTCACTGC GACAGCECCA GCCAACCAT CGGGGGCAAG TACTGTCTGG GTAGAGGAAG CGCGCACCG  
GGAGAGATC GGCAGTGCAC CTGTCGGGT CGGGTTGGA GCCCCGCTTC ATGACAGACCC CACTCTCTC CGCGCTGCC

+1 S C N T D D C P P G S Q D F R E V Q C S E F D S I P F  
 TSP1 Motif

=====

1921 TCCTGCAACA CGGATGACTG TCCCCCTGGC TCCCAAGACT TCAGAGRAAGT GCAGTGTCT GAAITTGACA GCATCCCTT  
AGGACGTGT GCCTACTGAC AGGGGGACCG AGGGTCTGA AGTCTCTCA CGTCACAAAGA CTTAAACTGT CGTAGGGAAA

+1 R G K F Y T K W K T Y R G G G V V K A C S L T C L A E G  
 2001 CGCTGGGGAAA TTCTACAAAGT GGAAACCTA CGGGGGAGGG GCGTGTAGGG CCTCTCGCT CACCTGCTA CGGGAGGCT  
CGCCACCTT AAGATGTTCA CCTTTGCTA CGCCCTCTCC CGCCGACTTCC GGACGAGCGA GTGACGGAT CGCCCTGCC

+1 F N F Y T E R A A A V V D G T P C R P D T V D I C V S  
 2081 TCAACTCTA CACGGAGAGG CGGGCAGCGC TGGTGGAGGG GACACCTGC CGTCCAGACA CGGTGGACAT TTGCGTCAGT  
AGTTGAAGAT GTCCCTCTCC CGCCGTCGGC ACCACCTGCC CTGTCGGACCG AGACTGTGA GCAACCTGTA AACCGAGCTCA

+1 G E C K H V G C D R V L G S D L R E D K C R V C G G D  
 2161 GGCGAATGCA AGCACGTGGG CTGCGACCGA TGCTGGGGT CCAGACCTGC GGAGGACAAG TCCCGACTGT GTGGCGGTGA  
CCGCTTAGCT TCGTCGACCC GACGTGGCT CAGGACCGGA GCGTGGACGC CCTCTGTTC ACGGCTCACCA CACCGCCAC

+1 G S A C E T I E G V F S P A S P G A G Y E D V V W I  
 2241 CGGCAGTGC TGCGAGACCA TCGAGGGCGT CTTCAGCCCA GCCTCACCTG GGGCGGGTA CGAGGATGTC GTCTGGATTC  
GGCGTCACCG AGCCTCTGGT AGCTCCCGCA GAAGTGGGT CGGAGTGGAC CCCGGCCCAT GCTCTACAG CAGACCTAAC

+1 P K G S V H I F I Q D L N L S L S H L A L K G D Q E S  
 2321 CCAAAGGCTC CGTCCACATC TTCTACAGG ATCTGAACCT CTCTCTCAGT CACTTGGCCC TGAAGGGAGA CCAGGAGTC  
GGTTCCGAG CGAGTGTAG AAGTAGGTCC TAGACTGGA GAGAGAGTC GTGAAACGGG ACTTCCCTCT GGTCTCAGG

+1 L L E G L P G T P Q P H R L P L A G T T F Q L R Q G  
 2401 CTGCTGCTGG AGGGGCTGCC CGGGACCCCC CAGCCCCACC GTCTGGCTCT AGCTGGACCC ACCTTCAAC TGCGACAGGG  
GACGACGACC TCCCCGACGG CCCCTGGGG GTCGGGGTGG CAGACGGAGA TGACCCCTGG TGGAAAGTT ACGCTGTCCC

+1 P D Q V Q S L E A L G P I N A S L I V M V L A R T E  
 2481 CGCAGACOAG GTCCAGAGCC TCGAAGCCCT GGGACCGATT AATGCACTTC TCATCGTCAT GGTGCTGGC CGGACCGAGC  
CGGTCTGGTC CAGGCTCGG AGCTTCCGG A CCTGGCTAA TTACGTAGAG AGTAGCAGTA CCACGACCGG GCCTGGCTGC  
  
 +1 L P A L R Y R F N A P I A R D S L P P Y S W H Y R P N  
TSP1-like Motif  
  
 2561 TGCCTGCCCT CCGCTACCGC TTCAATGCC CCATCGCCG TGACTCGCTG CCCCCCTACT CCTGGCACTA TSGCGCCCTCG  
ACGGACGGGA GGCATGGC AAGTTACGGG GTAGCGGC ACTGAGCGAC GGGGGATGA GGACCGATGA ACGGGGAGC  
  
 +1 T K C S A Q C A G G S Q V Q A V E C R N Q L D S S I V  
TSP1-like Motif  
  
 2641 ACCAAGTGT CGGCCCTAGTG TGCAGGGCGGT AGCCAGGTGC AGGCAGTGGGA GTGCCGCAAC CAGCTGGACA GCTCCGGCT  
TGGTTCACGA GCGGGTCAAC CGTCCGGCA TCGGTCACG TCCGGCACCT CACGGCGTTG CTGACCTGT CGGGGGGG  
  
 +1 A P H Y C S A H S K L P K R Q R A C N T E P C P P D  
TSP1-like Motif  
  
 2721 CGCCCCCAC TACTGCAGTG CCCACAGCAA GCTGCCAAAGGCGAGCGG CCTGCAACAC GGACCTGTG CCTCCAGACT  
GCGGGGGGTG ATGACGTCAC GGGTGTGTT CGCGTGCACG GGACGGTTT TCCGTCGCGC GGACGTTGTG CCTCGAACG GGAGGTCG  
  
 +1 W V V G N W S L C S R S C D A G V R S R S V V C Q R R  
TSP1-like Motif  
  
 2801 GGGTTGTAGG GAATGCTCG CTCTGCAGCC GCAGCTGGGA TCGAGGCCTG CGCAGCCGCT CGGTCTGTG CGAGCCCGCC  
CCCAACATCC CTTGACCAGC GAGACGTCGG CGTGCACGCT ACGTCGCAC GCGTCGGCGA GCCAGCACAC GGTGCGCGCG  
  
 +1 V S A A E E K A L D D S A C P Q P R P P V L E A C H G  
TSP1-like Motif  
  
 2881 CTCTCTGCCG CGGAGGAGAA GGCCTGGAC GACAGGGCAT GCCCCCAGCC GGGCCACCT GTACTGGAGG CCTGCCACCG  
CAGAGACGGC GCTCCCTCTT CGCGGACCTG CTGTCGCGTA CGGGCGTCGG CGGGGGTGGA CATGACCTCC GGACGGTGC  
  
 +1 P T C P P E W A A L D W S E C T P S C G P G L R H R  
TSP1-like Motif  
  
 2961 CCCCCACTGCA CCTCCGGAGT GGGCGGCCCT CGACTGCTT GAGTGCACCC CCAGCTGGGG GCGGGGCCCT CGCCACCGG  
GGGTGAACG GGAGGCTCA CCCCGGGGA GCTGACAGA CTCACGTGGG GTGCGACGCC CGGCCCGGAG CGGTGGCGC  
  
 +1 V V W L C K S A D H R A T L P P A H C S P A A K P P A T  
TSP1-like Motif  
  
 3041 TGGTCCTTG CAAGAGGCCA GACCACCGCG CCACGCTGCC CCCGGCCAC TGGTCAACCGG CGCCCAAGCC ACCGGCCAC  
ACCAGGAAAC GTTCTCCGT CTGGTGGCGC GTGCGACCG GGGCCCGTGTG ACCAGTGGGC GGCGGTTGG TGGCJGSTGG  
  
 +1 M R C N L R R C P P A R W V A G E W G E C S A Q C G V  
TSP1-like Motif  
  
 3121 ATGCGCTGCA ACTTGCGCG CTGCCCCCG GCGCGCTGGG TGGCTGGCA GTGGGGTGGAG TGCTCTGAC AGTGGGGGT  
TACCGACGT TGAACGGGGC GACGGGGGC CGGGCACCC ACCGACCGCT CACCCCACTC ACGAGACGTG TCAAGCCGCA

+1 G Q R Q R S V R C T S H T G Q A S H E C T E A L P F  
TSP1-like Motif

=====

3201 CGGGCAGGGG CAGGGCTCGG TGGCCTGCAC CAGCCACACG GGGCAGGGGT CGCACGAGTG CACGGAGGCC CTGGCGGCCG  
SCCCGTCGCC GTCGCGAGCC AC CGCAGCTG GTCGGTGTC CGCGTCCGCA CGCTGCTCAC GTGCCTCCGG GAGGCGCG

+1 P T T T Q Q C E A K C D S P T P G D G P E E C K D Y N  
TSP1-like Motif

=====

3281 CGACTACAC GCAGCAGTGT GAGGCCAAGT GGACAGCCC AACCCCGGGG GACGCCCTG AAGAGTGCAGA GGATGTGAC  
GCTGATGGTG CGTCGTCACA CTCCGGTTCA CGCTGTCGGG TTGGGGGCCG CTGGCGGGAC TTCTCACGTT CCTTCACGTC

+1 K V A Y C P L V L K F Q F C S R A Y F R Q M C C F T C  
3361 AAGGTCGCT ACTGCCCTC GGTGCTAAA TTCAGTTCT GAGGCCAGC CTACTCCGC CAGATGTGCT GCAAAACCTG  
TTCAGCGGA TGACGGGGGA CCACCGAGTT AAAGTCAGA CGTCGGCTCG GATGAAGGGG GTCTACACGA CGTTTGGAC

+1 Q G H

3441 CCAGGGCCAC TAGGGGGCGC GCGGCACCCG GAGGCCACAGC TGGCGGGTC TCCGCCGCCA GCCCTGCAGC GGGCGCGCG  
GGTCCCGGTG ATCCCCCGG CGCCGTTGGC CTCGGTGTCG ACCGCCCGAG AGGGGGGGT CGGGACGTCG CCCGGCCGGT

3521 GAGGGGGGCC CGGGGGGGGC GGGAACTGGG AGGGAGGGT GAGACGGAGC CGGAAGTTAT TTATGGAA CCCCTGCAGG  
CTCCCCCGG GCCCCCCCCG CCCTTGTCCC TCCCTTCCC CTCTGCCTCG GCCTCAATA AATAACCCCTT GGGGACGTC

3601 GCCCTGGCTG GGAGGATCCA CCCAACCTC TGCCCTGCC GCCCCAGGGG CACCCGACA TCCAGGCCAC CCCCTCATGG  
CGGGACCGAC CCTCTAGGT GGGGTTGGAG ACGGGACGGG CGGGGTCCC GTGGGGTGT AGGTCCGGTG GGGGASTAC

3681 TGCTACAGAC CCTGCCCTGG GGCCCACACA CTCCCTGCCAG GAAGCCCTAC ATCAATAAG TTCTGCTTG TGTAGATTG  
ACGATGTCTG GGACGGGACC CGGGGTGTGT GAGGACGGTC CTTCGGGATG TAGTTATTC AAGRCAAAAC ACATCTAAAG

3761 TAAAAAAA AAAA  
ATTTTTTTT TTTTT

Metalloproteinase Domain Alignment of ADAMTS-E v. ADAMTS Family

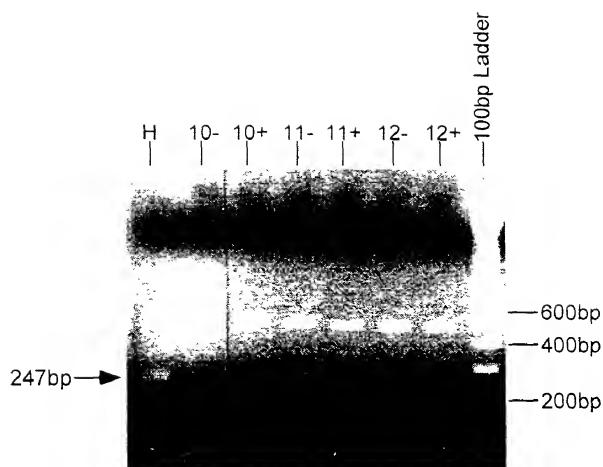


Figure 5. Expression of ADAMTS-E in cDNA from osteoarthritic cartilage.

**Figure 6. Amino acid alignment of human ADAMTS-E with a GenScan prediction of ADAMTS-E from mouse genomic sequence.**

hADAMTS-E	1 -----HASSGAERPGAAQEGG---DAAKAVNRGGGTGVAAGSRGWGETCGHVASMAPACQILRWALALG (1) XMCDSHSYSPPFVPLLLRVRNGQCLPHKVDVKGTSDAAQTVNRGGSTVGAASSRGWGETCGHVAPMASACQILRWALALG Consensus (1) G P G DAA VNRRGG TVGAA SRGWGETCGHVA MA ACQILRWALALG	20
mADAMTS-E	81 (62) LGLMFVEVTHAFRSQDEFLLSLESYEIAFPTRVDHNGALLAFLSFSSPPPRQRRTGATAESRLFYKVASPSTHFLNLTPSS (81) GLUTFKVTHAFRSODELLSLESYEIAFPTRVDHNGAMLAFLSPFAFRQRGRGATTESLRFYKVAPSTHFLNLTRP Consensus (81) LGL F VTHAFRSQDE LSSESLEYIAFPTRVDHNGA LAFSPP RRQRGG GAT ESRLFYKVA PSTHFLNLTPS	160
hADAMTS-E	161 (142) RLLAGHVSVEYWTREGLAWQRAARPHCLYAGHLQGQASTSHVAISTCGLLHGLIVADEEYIEPLHGGPKGSRSPEESG mADAMTS-E (161) RLLAGHVSVEYWTREGLAWQRAARAHCLYAGHLQGQAGSSHVAVSTCGGLHGLIVADEEYIEPLQGGPKGHRGPEESG Consensus (161) RLLAGHVSVEYWTREGLAWQRAAR HCLYAGHLQGQA SHVA STCGGLHGLIVAD EYIEPL GGPK R PEESG	240
hADAMTS-E	241 (222) PHVYVKRSSLRHPHLDTAGCVRDEPKWKGRPWVLTLKPPPAPLGNETERGQPGLKRSVSRERYVETLVADKMMVAYH mADAMTS-E (241) PHVYVKRSSLRHPHLDTAGCVRDEPKWKGRPWVLTLKPPPARELGNESERGQQLGKLRSVSRERYVETLVADKMMVAYH Consensus (241) PHVYVKRSSLRHPHLDTAGCVRDEPKWKGRPWVLTLKPPPAPLGNE ERGQ GLKRSVSRERYVETLVADKMMVAYH	320
hADAMTS-E	321 (302) GRDVQEYVVLAIMNIV-----AKLFQDSSLGISTVNILVTRLILLTEDOPTLEITHHAGKSLDSFCWKQKSIVVNS mADAMTS-E (321) GRDVQEYVVLAIMNITRSLLFLGGQVAKLFQDSSLGISTVNILVTRLILLTEDOPTLEITHHAGKSLDSFCWKQKSIVVNS Consensus (321) GRDVQEYVVLAIMNI AKLFQDSSLG VNILVTRLILLTEDOPTLEITHHAGKSLDSFCWKQKSIVVNS	400
hADAMTS-E	401 (372) GHGNAPIENGVANHDATAVLITYRDIC1YKNNPCGTGLGAPVGGMCERERSCSVNEDIGLATAFTIAHEIGHTFGMHNHDGV mADAMTS-E (401) GHGNAPIENGVANHDATAVLITYRDIC1YKNNPCGTGLGAPVGGMCERERSCSINEDIGLATAFTIAHEIGHTFGMHNHDGV Consensus (401) GHGNAPIENGVANHDATAVLITYRDIC1YKNNPCGTGLGAPVGGMCERERSCS NEDIGLATAFTIAHEIGHTFGMHNHDGV	480
hADAMTS-E	481 (452) GNSCGARGQDPAKLMAAHITMKTNFVWSSCSRDIYTSLFDSLGLCLNNRPPRQDFVYPTVAPGQAYDADEQCRFQHG mADAMTS-E (481) GNNGCARGQDPAKLMAAHITMKTNFVWSSCSRDIYTSLFDSLGLCLNNRPPRQDFVYPTVAPGQAYDADEQCRFQHG Consensus (481) GN CGARGQDPAKLMAAHITMKTNFVWSSCSRDIYTSLFDSLGLCLNNRPPRQDFVYPTVAPGQAYDADEQCRFQHG	560
hADAMTS-E	561 (532) KSRQCKYGEVCSELWCLSKSNRCITNSI PAAEGTLQCHTIDKGWCYKRVCPFGSPLPEGVGDANGFWTFGDSRCTGG mADAMTS-E (561) KSRQCKYGEVCSELWCLSKSNRCITNSI PAAEGTLQCHTIDKGWCYKRVCPFGSPLPEGVGDANGFWTFGDSRCTGG Consensus (561) KSRQCKYGEVCSELWCLSKSNRCITNSI PAAEGTLQCHTIDKGWCYKRVCPFGSPLPEGVGDANGFWTFGDSRCTGG	640
hADAMTS-E	641 (612) GVSSSSRHCDSPRPTIGGYKCLGERRRHRSCTNDCCPPGSQDFREVCQCEFDSDIPFRGKFYKWKTYRGGGVKACSLTCLA mADAMTS-E (641) GVSSSSRHCDSPRPTIGGYKCLGERRRHRSCTNDCCPPGSQDFREVCQCEFDSDIPFRGKFYWTKYRGGGVKACSLTCLA Consensus (641) GVSSSSRHCDSPRPTIGGYKCLGERRRHRSCTNDCCPPGSQDFREVCQCEFDSDIPFRGKFY WTQYRGGGVKACSLTCLA	720
hADAMTS-E	721 (692) EGFNFTTERAAA VV DGTPCRDTVDICVSGECKHVGCDRVLGSLDRDKECRVCGGDSACETIEGVFSPPASPGAGYDEVV mADAMTS-E (721) EGFNFTTERAAA VV DGTPCRDTVDICVSGECKHVGCDRVLGSLDRDKECRVCGGDSACETIEGVFSPPALPGTYDEVV Consensus (721) EGFNFTTERAAA VV DGTPCRDTVDICVSGECKHVGCDRVLGSLDRDKECRVCGGDSACETIEGVFSPPA PG GYDEVV	800
hADAMTS-E	801 (772) WIPKGSHVIFIQDLNLSLSSLHSLALKGDQESLLELGLPGTPQPHRPLLAGTTFOLRQGDQVQSLEALGPINASLIMVLLAR mADAMTS-E (801) WIPKGSHVIFIQDLNLSLSSLHSLALKGDQESLLELGLPGTPQPHRPLLAGTTFHLRQGDQVQSLEALGPINASLIMVLLAQ Consensus (801) WIPKGSHVIFIQDLNLSLSSLHSLALKGDQESLLELGLPGTPQPHRPLLAGTTF LRQGDQV QSLEALGPINASLIMVLLAQ	880
hADAMTS-E	881 (852) AELPALBYRFNAPIARDLPPYSWYAPWTKCSAQCAAGGSQVQAVECRNQLDSSAVAPHYCSAHSKLPKRQRACNTTECP mADAMTS-E (881) AELPALHYRFNAPIARDLPPYSWYAPWTKCSAQCAAGGSQVQVECRNQLDSSAVAPHYCSGHSKLPKRQRACNTTECP Consensus (881) ELPAL YRFNAPIARD LPPYSWYAPWTKCSAQCAAGGSQVQ VECRNQLDSSAVAPHYCS HSMLPKRQRACNTTECP	960
hADAMTS-E	961 (932) PDWWVGNWSLCSRSRCDAGVRSRSVVCQRRVSAEEKALDDSACPQPRPPVLEACHGPTCPPEWAALDWSECTPSCCPGLR mADAMTS-E (961) PDWWVGNWSRCSRSRCDAGVRSRSVVCQRRVSAEEKALDDSACPQPRPPVLEACCGPMPCEWEATLDWSECTPSCCPGLR Consensus (961) PDWWVGNWS CSRSRCDAGVRSRSVVCQRRVSAEEKALDDSACPQPRPPVLEAC GP CPPEWA LDWSECTPSCCPGLR	1040

RADAMTS-E (1012) HRVVVLCKSADHRATLPPAHCSPAAKPPATMRCNLRRCPPARWVAGEWGECSAQCGVGQQRORSVRCTSHTGQASRECTEAL  
RADAMTS-E (1041) HRVVVLCKSADQRSTLPBGHCLPAAKPSTMRCNLRRCPPARWVSEWGECS---GLQQQORTVRCTSHTGQPSPRECTEAL  
Consensus (1041) HRVVVLCKSAD R TLPP HC PAAKPP TMRCNLRRCPPARWV EWGEC G GQ QR VRCTSHTGQ S ECTEAL

1121

1180

RADAMTS-E (1092) RPPTTTQQCEAKCDSPTP-GDGPEECKDVNKVAYCPLVLKFQFCSRAYFRQMCCKTQGH  
RADAMTS-E (1117) R-PSTMQQCEAKCDSVVPGDPEECKDVNKVAYCPLVLKFQFCSRAYFRQMCCKTQGR  
Consensus (1121) R P T QQCEAKCDS P GDGPEECKDVNKVAYCPLVLKFQFCSRAYFRQMCCKTQG